

claim 31 is allowed. By this Amendment, Figs. 1, 3 and 4 are amended; the specification is amended; claims 4, 29 and 30 are canceled; claims 1 and 9 are amended; and claims 32-56 are added. No new matter is added.

The attached Appendix includes marked-up copies of each rewritten paragraph (37 C.F.R. §1.121(b)(1)(iii)) and claim (37 C.F.R. §1.121(c)(1)(ii)).

Entry of the amendments is proper under 37 CFR §1.116 since the amendments: (a) place the application in condition for allowance (for the reasons discussed herein); (b) do not raise any new issue requiring further search and/or consideration (since the amendments amplify issues previously discussed throughout prosecution); (c) satisfy a requirement of form asserted in the previous Office Action; and (d) place the application in better form for appeal, should an appeal be necessary. The amendments are necessary and were not earlier presented because they are made in response to arguments raised in the final rejection. Entry of the amendments is thus respectfully requested.

The attached paper copy and computer-readable copy of the Sequence Listing are submitted in compliance with 37 C.F.R. §§1.821-1.825. The contents of the paper copy and the computer-readable copy of the Sequence Listing are the same. No new matter is added. Support for the information provided in the Sequence Listing can be found in the original Sequence Listing and Figures.

#### **I. CLAIM AMENDMENTS AND NEW CLAIMS**

Amended claim 1 and new claims 33 and 38 pertain to SEQ ID NO:1 (AtRDP3A), support for which may be found, at least, at Figures 1A and 9, and Example 2 at page 39, line 30 to page 40, line 2, of the specification.

Amended claims 1 and 9 and new claims 34, 39, 42 and 45 pertain to SEQ ID NO:3 (AtRDP3B), support for which may be found, at least, at Figure 1B (coding region extends

from nucleotide 121-1533), Figure 3 (homology determination between SEQ ID NO's:1 and 3), and Example 1, page 37, lines 21-28 of the specification.

Amended claims 1 and 9 and new claims 35, 40, 43, 46 and 48-50 recite full length and specific fragments of SEQ ID NO:5, support for which may be found, at least, at Figures 10 and 2A, and page 27, line 28 to page 28, line 9 of the specification (also see table below).

Amended claims 1 and 9 and new claims 36, 41, 44, and 51-56 recite full length and specific fragments of SEQ ID NO:7, support for which may be found, at least, at Figures 4 and 2B, and page 37, line 30 to page 38, line 8 of the specification (also see table below).

For the Examiner's convenience, the following table identifies the nucleotide numbering of AtHD2A and AtHD2B (SEQ ID NO's:5 and 7, respectively; identified in the amended claims) that corresponds with the amino acid numbering in Figure 10, using the data presented in Figure 2A.

AtHD2A		AtHD2B	
Amino acid*	Nucleic acid** (SEQ ID NO:5)	Amino acid***	Nucleic acid**** (SEQ ID NO:7)
1	49	1	61
73	267	72	276
137	457	154	522
162	534	198	655
211	681	265	855
245	783	305	975

\*amino acid numbering obtained from Figure 10

\*\* nucleotide numbering correlated to amino acid numbering using Figure 2A

\*\*\* amino acid numbering obtained from correlation of AtHD2B and AtHD2A amino acids sequences shown in Figure 4

\*\*\*nucleotide numbering correlated to amino acid numbering according to Figure 2B.

## **II. OBJECTIONS TO THE DRAWINGS**

The Office Action objects to substitute Figure 4, which was submitted to the Patent Office in the September 9, 2002 Amendment, asserting that an underline that appears in the new Figure 4 at amino acids 200-238 of the ZmHD2 sequence is at a different position than in the original Figure 4, in which the underline appears at amino acids 150-195 of the ZmHD2 sequence. Applicants note that Figure 4 as originally filed included the underlining from amino acids 150-196 of the ZmHD2 sequence. A corrected Figure 4 attached hereto places a line under amino acids 150-196 of the ZmHD2 sequence and removes the line going through amino acids 200-238 of the ZmHD2 sequence, which is identical to the line placement found in original Figure 4.

In addition, Figures 1, 3 and 4 have been amended to correct clerical errors, including clerical errors in amino acid numbering. In particular, Figure 3 has been amended to remove a valine (V) residue at position 11 of the AtRPD3A sequence. As amended, the AtRPD3A sequence shown in Figure 3 is consistent with the AtRPD3A sequence shown in Figure 1A and SEQ ID NO:2 as originally filed. Figure 3 has been further amended to correct the prior art sequence of ZmRPD3. This correction replaces a glutamine (Q) with a glutamate (E) residue at position 181 of the (prior art) sequence of ZmRPD3. Figure 4 has been amended to correct the prior art sequence ZmHD2. This correction inserts a serine (S) residue at position 34 of the prior art sequence ZmHD2.

Reconsideration and withdrawal of the objection and approval of drawing corrections are respectfully requested.

**III. OBJECTIONS TO THE SPECIFICATION**

The Office Action objects to the Specification because the Sequence Listing does not include the sequences found in Figures 3 and 4, and because the brief descriptions of Figures 3 and 4 do not include SEQ ID NO's for the described sequences. Applicants concurrently file a new Sequence Listing that includes the sequences listed in Figures 3 and 4, and have amended the brief descriptions of Figures 3 and 4 to indicate the corresponding SEQ ID NO's for the ZmRPD3, RPD3, and ZmHD2 sequences. The Sequence Listing has been further amended to correct clerical errors in SEQ ID NO:7, such that it now sets forth a sequence that is identical to the sequence depicted in Figure 2B as originally filed. The amended Sequence Listing does not go beyond the disclosure in the present application, as originally filed.

Reconsideration and withdrawal of the rejection are respectfully requested.

**IV. CLAIM REJECTIONS UNDER 35 U.S.C. §112, SECOND PARAGRAPH**

The Office Action rejects claims 9, 11-13, 17-19 and 29 under 35 USC §112, second paragraph, as being indefinite. In particular, the Office Action in paragraph 8 has raised several objections to the terms "deletion", "fragment", and to the phrase "a nucleotide sequence that is at least 80% identical".

Claim 29 has been cancelled without prejudice or disclaimer. Therefore the rejection against this claim is now moot.

Claim 9 is amended so that it does not recite the terms "deletion," "fragment," or the phrase "a nucleotide sequence that is at least 80% identical." Claims 11-13 and 17-19 do not recite these terms, and are merely rejected as depending from claim 9. Accordingly, all of claims 9, 11-13 and 17-19 satisfy the requirements of §112, second paragraph.

Reconsideration and withdrawal of the rejection are respectfully requested.

**V. CLAIM REJECTIONS UNDER 35 U.S.C. §112, FIRST PARAGRAPH**

The Office Action rejects claims 1-9, 11-19, 29 and 30 under 35 U.S.C. §112, first paragraph, as failing to meet the written description and enablement requirements. In particular, the Office Action in paragraphs 9 and 10 (and in the previous Office Action, paper no. 13) indicates that the specification does not support or enable the terms "deletion," "fragment," or the phrase "a nucleotide sequence that is at least 80% identical."

Claims 29 and 30 have been cancelled without prejudice or disclaimer. Therefore, the rejection against these claims is now moot.

As discussed above in Section IV, claims 1 and 9 have been amended to remove the objectionable language and to recite specific nucleotide sequences that are explicitly supported by the specification. The claimed nucleotide sequences are defined both by structure (i.e., specific nucleotide sequences disclosed in the Figures and Sequence Listing) and function (i.e., hybridization under defined conditions and encoding a product that exhibits repression of gene expression activity). For at least these reasons, claims 1 and 9 satisfy the written description and enablement requirements of §112, first paragraph.

Claims 2-8 and 11-19 do not recite the objectionable language, and are rejected as depending from claim 1 or claim 9. Claims 2-8 and 11-19 further narrow claim 1 or claim 9, and thus satisfy the written description and enablement requirements of §112, first paragraph, for at least the same reasons as claim 1 and claim 9.

Reconsideration and withdrawal of the rejection are respectfully requested.

**VI. CLAIM REJECTIONS UNDER 35 U.S.C. §103**

The Office Action rejects claims 1-3, 5-8 and 14-16 under 35 U.S.C. 103(a) as being unpatentable over WO 98/48825 to Evans et al. (Evans) in combination with U.S. Patent No. 6,287,843 to Baldwin et al. (Baldwin). Claims 1-3, 5-8 and 14-16 are patentable over the cited references for at least the reasons discussed below.

Claim 1 as presently amended recites nucleotide sequences of AtHD2A (SEQ ID NO:5), AtHD2B (SEQ ID NO:7), AtRPD3A (SEQ ID NO:1) and ATRPD3B (SEQ ID NO:3), and sequences that hybridize to AtHD2A (SEQ ID NO:5), AtHD2B (SEQ ID NO:7), AtRPD3A (SEQ ID NO:1) and ATRPD3B (SEQ ID NO:3) under defined hybridization conditions. Applicants submit that neither Evans nor Baldwin teach or suggest any of the claimed sequences, and therefore claim 1 is patentable over Evans, alone or in view of Baldwin. Claims 2-3, 5-8,14-16 ultimately depend from claim 1, and thus include all of its limitations. Accordingly, these dependent claims are patentable over the cited references for at least the same reasons as claim 1.

Reconsideration and withdrawal of the rejection are respectfully requested.

**VI. ALLOWED CLAIM**

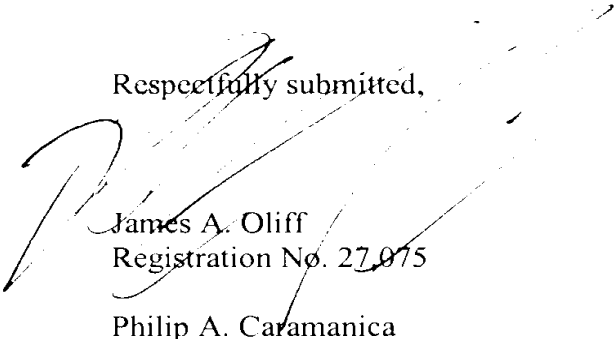
Applicants appreciate the indication that claim 31 has been allowed.

**VII. CONCLUSION**

In view of the foregoing amendments and remarks, Applicants submit that this application is in condition for allowance. Favorable reconsideration and prompt allowance of claims 1-3, 5-9, 11-19 and 31-56 are earnestly solicited.

Should the Examiner believe that anything further would be desirable in order to place this application in better condition for allowance, the Examiner is invited to contact Applicants' undersigned representative at the telephone number set forth below.

Respectfully submitted,

  
James A. Oliff  
Registration No. 27,075

Philip A. Caramanica  
Registration No. 51,528

JAO:PAC/jam

Attachment:

Appendix  
Sequence Listing (paper and computer-readable copies)  
Request for Approval of Drawing Corrections

Date: February 20, 2003

**OLIFF & BERRIDGE, PLC**  
**P.O. Box 19928**  
**Alexandria, Virginia 22320**  
**Telephone: (703) 836-6400**

<p>DEPOSIT ACCOUNT USE AUTHORIZATION Please grant any extension necessary for entry; Charge any fee due to our Deposit Account No. 15-0461</p>
--

## APPENDIX

## Changes to Specification:

The Sequence Listing is replaced.

Page 7, lines 16-24:

**FIGURE 3** displays the amino acid sequence alignment of the *AtRPD3A* (SEQ ID NO:2), *AtRPD3B* (SEQ ID NO:4), maize RPD3 (ZmRPD3; SEQ ID NO:12) and yeast RPD3 (SEQ ID NO:13). Identical amino acids are shaded in black. The amino acids with asterisks represent residues with potential roles in deacetylase activity.

**FIGURE 4** displays the amino acid sequence alignment of AtHD2A (SEQ ID NO:6), AtHD2B (SEQ ID NO:8) and maize HD2 (ZmHD2; SEQ ID NO:14). Identical amino acids are shaded in black. The amino acids with asterisks are the predicted histone deacetylase catalytic residues. The extended acidic domains are underlined.

## Changes to Claims:

Claims 4, 29 and 30 are canceled.

Claims 32-56 are added.

The following is a marked-up version of the amended claims:

1. (Twice Amended) A method of repressing transcription of a coding sequence of interest in a transgenic plant, comprising:
  - a) introducing into a plant:
    - i) a first chimeric nucleotide sequence comprising a first regulatory element in operative association with a gene of interest, and a controlling sequence; and
    - ii) a second chimeric nucleotide sequence comprising a second regulatory element in operative association with a nucleotide sequence encoding a histone



deacetylase fused with a DNA binding protein, said DNA binding protein interacting with said controlling sequence, to produce said transgenic plant; and

\_\_\_\_\_ b) growing said transgenic plant;

\_\_\_\_\_ wherein said nucleotide sequence encoding a histone deacetylase is selected from the group consisting of:

\_\_\_\_\_ *AtRPD3A*, a nucleotide sequence that hybridizes to *AtRPD3A* under a hybridization condition,

\_\_\_\_\_ *AtRPD3B*, a nucleotide sequence that hybridizes to *AtRPD3B* under a hybridization condition,

\_\_\_\_\_ *AtHD2A*, a nucleotide sequence that hybridizes to *AtHD2A* under a hybridization condition,

\_\_\_\_\_ *AtHD2B*, a nucleotide sequence that hybridizes to *AtHD2B* under a hybridization condition,

\_\_\_\_\_ nucleotides 1-1807 of SEQ ID NO:1, a nucleotide sequence that hybridizes to nucleotides 1-1807 of SEQ ID NO:1 under a hybridization condition,

\_\_\_\_\_ nucleotides 142-1644 of SEQ ID NO:1, a nucleotide sequence that hybridizes to nucleotides 142-1644 of SEQ ID NO:1 under a hybridization condition,

\_\_\_\_\_ nucleotides 1-1800 of SEQ ID NO:3, a nucleotide sequence that hybridizes to nucleotides 1-1800 of SEQ ID NO:3 under a hybridization condition,

\_\_\_\_\_ nucleotides 121-1533 of SEQ ID NO:3, a nucleotide sequence that hybridizes to nucleotides 121-1533 of SEQ ID NO:3 under a hybridization condition,

\_\_\_\_\_ nucleotides 1-939 of SEQ ID NO:5, a nucleotide sequence that hybridizes to nucleotides 1-939 of SEQ ID NO:5 under a hybridization condition,

\_\_\_\_\_ nucleotides 49-783 of SEQ ID NO:5, a nucleotide sequence that hybridizes to nucleotides 49-783 of SEQ ID NO:5 under a hybridization condition,

nucleotides 49-681 of SEQ ID NO:5, a nucleotide sequence that hybridizes to nucleotides 49-681 of SEQ ID NO:5 under a hybridization condition,

nucleotides 49-534 of SEQ ID NO:5, a nucleotide sequence that hybridizes to nucleotides 49-534 of SEQ ID NO:5 under a hybridization condition,

nucleotides 49-267 and 457-534 of SEQ ID NO:5, a nucleotide sequence that hybridizes to nucleotides 49-267 and 457-534 of SEQ ID NO:5 under a hybridization condition,

nucleotides 1-1212 of SEQ ID NO:7, a nucleotide sequence that hybridizes to nucleotides 1-1212 of SEQ ID NO:7 under a hybridization condition,

nucleotides 61-975 of SEQ ID NO:7, a nucleotide sequence that hybridizes to nucleotides 61-975 of SEQ ID NO:7 under a hybridization condition,

nucleotides 61-855 of SEQ ID NO:7, a nucleotide sequence that hybridizes to nucleotides 61-855 of SEQ ID NO:7 under a hybridization condition,

nucleotides 61-655 of SEQ ID NO:7, a nucleotide sequence that hybridizes to nucleotides 61-655 of SEQ ID NO:7 under a hybridization condition,

nucleotides 61-276 and 522-655 of SEQ ID NO:7, and a nucleotide sequence that hybridizes to nucleotides 61-276 and 522-655 of SEQ ID NO:7 under a hybridization condition;

wherein each said hybridization condition is selected from the group consisting of:

hybridization in 4XSSC at 65°C, followed by washing in 0.1XSSC at 65°C for an hour,

hybridization in 50% formamide and 4XSSC at 42°C, followed by washing in 0.1XSSC at 65°C for an hour, and

hybridization in 0.5 M Na<sub>2</sub>HPO<sub>4</sub> (pH 7.2), 7% SDS, and 1mM EDTA at 65°C, followed by washing for 15 minutes in 2 x SSC with 0.1% SDS at room temperature, then washing twice for 20 minutes in 0.1 x SSC, 0.1% SDS at 65°C; and

wherein said nucleotide sequence that hybridizes encodes a product that exhibits repression of gene expression activity.

9. (Twice Amended) An isolated nucleotide sequence, selected from the group consisting of:

- i) SEQ ID NO:3, SEQ ID NO:5, or SEQ ID NO:7;<sub>3</sub>
- ii) ~~a deletion or fragment of SEQ ID NO:3, SEQ ID NO:5, or SEQ ID NO:7; and~~
- ~~iii) a nucleotide sequence that hybridizes to SEQ ID NO:3, SEQ ID NO:5, or SEQ ID NO:7,~~
- iii) a nucleotide sequence that hybridizes to nucleotides 1-1800 of SEQ ID NO:3 under a hybridization condition,
- iv) nucleotides 121-1533 of SEQ ID NO:3,
- v) a nucleotide sequence that hybridizes to nucleotides 121-1533 of SEQ ID NO:3 under a hybridization condition,
- vi) nucleotides 1-939 of SEQ ID NO:5,
- vii) a nucleotide sequence that hybridizes to nucleotides 1-939 of SEQ ID NO:5 under a hybridization condition,
- viii) nucleotides 49-783 of SEQ ID NO:5,
- ix) a nucleotide sequence that hybridizes to nucleotides 49-783 of SEQ ID NO:5 under a hybridization condition,
- x) nucleotides 49-681 of SEQ ID NO:5,

\_\_\_\_\_ xi) a nucleotide sequence that hybridizes to nucleotides 49-681 of SEQ ID NO:5 under a hybridization condition,

\_\_\_\_\_ xii) nucleotides 49-534 of SEQ ID NO:5,

\_\_\_\_\_ xiii) a nucleotide sequence that hybridizes to nucleotides 49-534 of SEQ ID NO:5 under a hybridization condition,

\_\_\_\_\_ xiv) nucleotides 49-267 and 457-534 of SEQ ID NO:5,

\_\_\_\_\_ xv) a nucleotide sequence that hybridizes to nucleotides 49-267 and 457-534 of SEQ ID NO:5 under a hybridization condition,

\_\_\_\_\_ xvi) nucleotides 1-1212 of SEQ ID NO:7,

\_\_\_\_\_ xvii) a nucleotide sequence that hybridizes to nucleotides 1-1212 of SEQ ID NO:7 under a hybridization condition,

\_\_\_\_\_ xviii) nucleotides 61-975 of SEQ ID NO:7,

\_\_\_\_\_ xix) a nucleotide sequence that hybridizes to nucleotides 61-975 of SEQ ID NO:7 under a hybridization condition,

\_\_\_\_\_ xx) nucleotides 61-855 of SEQ ID NO:7,

\_\_\_\_\_ xxi) a nucleotide sequence that hybridizes to nucleotides 61-855 of SEQ ID NO:7 under a hybridization condition,

\_\_\_\_\_ xxii) nucleotides 61-655 of SEQ ID NO:7,

\_\_\_\_\_ xxiii) a nucleotide sequence that hybridizes to nucleotides 61-655 of SEQ ID NO:7 under a hybridization condition,

\_\_\_\_\_ xxiv) nucleotides 61-276 and 522-655 of SEQ ID NO:7, and

\_\_\_\_\_ xxv) a nucleotide sequence that hybridizes to nucleotides 61-276 and 522-655 of SEQ ID NO:7 under a hybridization condition;

\_\_\_\_\_ wherein each said hybridization condition is selected from the group consisting of:

\_\_\_\_\_ hybridization in 4XSSC at 65°C, followed by washing in 0.1XSSC at 65°C for an hour,

\_\_\_\_\_ hybridization in 50% formamide and 4XSSC at 42°C, followed by washing in 0.1XSSC at 65°C for an hour, and

\_\_\_\_\_ hybridization at 65°C in 0.5 M Na<sub>2</sub>HPO<sub>4</sub> (pH 7.2), 7% SDS, and 1 mM EDTA at 65°C, followed by washing for 15 minutes in 2 x SSC with 0.1% SDS at room temperature, then twice washing for 20 minutes in 0.1 x SSC, 0.1% SDS at 65°C; and \_\_\_\_\_ wherein said ~~fragment, said deletion, or~~ said nucleotide sequence that hybridizes encodes a product that exhibits repression of gene expression activity.